

Query Match 71.8%, Score 7756.5, DB 1; Length 1569;
 Best Local Similarity 93.1%; Pred. No. 0;
 Matches 1553; Conservative 1; Mismatches 1; Indels 113; Gaps 3;

QY 1 MTSIAQOQIARLALPOSDSLSRDEVASLFDPRKAATIDDDTAATICTGLEELGDP 60
 DB 2 MTSIAQOQIARLALPOSDSLSRDEVASLFDPRKAATIDDDTAATICTGLEELGDP 61

QY 61 SFEQEPAPLFSQAKTLERSVOTKAVNKOLDENISLFIHLSPEFLKPAQCLEMLHR 120
 DB 62 SFEQEPAPLFSQAKTLERSVOTKAVNKOLDENISLFIHLSPEFLKPAQCLEMLHR 121

QY 121 FHIHLYNODSLIACVLPYHETRIEVRVIOQLKINNSKHEMFLPVKOGVPLAKGTLIT 180
 DB 122 FHIHLYNODSLIACVLPYHETRIEVRVIOQLKINNSKHEMFLPVKOGVPLAKGTLIT 181

QY 181 HCYKDLGFMDFICSLMYKSVKFAEYSSAQLVLAFASTYVSALVAEDVSDNTIA 240
 DB 182 HCYKDLGFMDFICSLMYKSVKFAEYSSAQLVLAFASTYVSALVAEDVSDNTIA 241

QY 241 KLFPIYIOGKLSLPDYRAATYMTICQISVRYTMENTEVSASQIITKTKIPSLIKDG 300
 DB 242 KLFPIYIOGKLSLPDYRAATYMTICQISVRYTMENTEVSASQIITKTKIPSLIKDG 301

QY 301 LSCILVILQKRPESLQK-----PPHLCNVPDLITLHGISETYDVSPL 347
 DB 302 LSCILVILQKRPESLQKRYVOLILRNQASQRPPLCNVVDLITLHGISETYDVSPL 361

QY 348 RYMLPHLVSIHHVTGETEGMDQIYKRLHLEILKISKNLMDHLASLEETYSY 407
 DB 362 HYMLPHLVSIHHVTGETEGMDQIYKRLHLEILKISKNLMDHLASLEETYSY 421

QY 408 SSOEEMSNKVSLLNEQFLPLRLLESKYPTLDVLEEHLEKELADIKQELFHOFSLS 467
 DB 422 SSOEEMSNKVSLLNEQFLPLRLLESKYPTLDVLEEHLEKELADIKQELFHOFSLS 481

QY 468 TSGKTYOFLADSDTSLMSLNHPRLAPRILAMNLKIKMSKGVDSPTKEAVLARLG 527
 DB 482 TSGKTYO-----GVDSEPTKEAVLARLG 505

QY 528 DDNDIVVLSAISAEIFEKHEHSEVITISNLLNLFORAEISKNGMEVYLKIAADILKEE 587
 DB 506 DDNDIVVLSAISAEIFEKHEHSEVITISNLLNLFORAEISKNGMEVYLKIAADILKEE 565

QY 588 ILSNDOLSNQVVCLLPFPVYINNDOTESAEMKIAIYLSKSGICSLHPLRGMEALENV 647
 DB 566 ILSNDOLSNQVVCLLPFPVYINNDOTESAEMKIAIYLSKSGICSLHPLRGMEALENV 625

QY 648 IKSTRPKGLIGVANKMIELLADININGDPSMKAWEDELISVEEESFNLKOKVTPHVI 707
 DB 626 IKSTRPKGLIGVANKMIELLADININGDPSMKAWEDELISVEEESFNLKOKVTPHVI 661

QY 708 LSVLVSCSSSLKETHFPFAIRVFSILOKIKKLESVITAVEIPSEMHIELMDGPIVEL 767
 DB 662 -----EIPSEMHIELMDGPIVEL 681

QY 768 WAHYVEELNSTQRAVAVDSVFLVFSLKFTYALKAPKSPKGDIMWPEOLKEDSRDYLA 827
 DB 682 WAHYVEELNSTQRAVAVDSVFLVFSLKFTYALKAPKSPKGDIMWPEOLKEDSRDYLA 741

QY 828 LLLGLFEMMLNGADAVHFRVLMKLEIVHLEEDVOLFQKPSVLMYTGSSISNPLNCVKT 887
 DB 742 LLLGLFEMMLNGADAVHFRVLMKLEIVHLEEDVOLFQKPSVLMYTGSSISNPLNCVKT 801

QY 888 VLQTOALYVCAMISQKTOCKHQALASISPVYTSLLINLSGPYKEVRAAIOCLALSG 947
 DB 802 VLQTOALYVCAMISQKTOCKHQALASISPVYTSLLINLSGPYKEVRAAIOCLALSG 861

QY 948 VASPEFYIIDLHLSKAETISDAAYVYODIATLFEELQREKKLKSQKISLTKMLSCV 1007
 DB 862 VASPEFYIIDLHLSKAETISDAAYVYODIATLFEELQREKKLKSQKISLTKMLSCV 921

QY 1008 YSCPSYIAKDLMLKVLQVNGEMVLSOLLPMAEOLLEKIOKEPTAVLKDEAMVHLTLGKY 1067
 DB 922 YSCPSYIAKDLMLKVLQVNGEMVLSOLLPMAEOLLEKIOKEPTAVLKDEAMVHLTLGKY 981

QY 1068 NEFSVSLNEDPKSLDIFINAVHTTKELVYAGMPTIOITALEKITKPPFAAISDEKVOOKL 1127
 DB 982 NEFSVSLNEDPKSLDIFINAVHTTKELVYAGMPTIOITALEKITKPPFAAISDEKVOOKL 1041

QY 1128 LRMLFDLLVNCNKHCAQOTVSSVFKGISVNAEOVRIELEPPDAKPLGTVQOKRQKMOQ 1187
 DB 1042 LRMLFDLLVNCNKHCAQOTVSSVFKGISVNAEOVRIELEPPDAKPLGTVQOKRQKMOQ 1101

QY 1188 KKSODLESVOEGSSYQORVTLLELLOHKKLRSQIIVPTLFLNLSRCLPELPQEOGN 1247
 DB 1102 KKSODLESVOEGSSYQORVTLLELLOHKKLRSQIIVPTLFLNLSRCLPELPQEOGN 1161

QY 1248 MEYTKOLILSCLNLCOKLSPPDGKIPKDLIDEEKFVVELIVOCIRLSEMPOTHHNALL 1307
 DB 1162 MEYTKOLILSCLNLCOKLSPPDGKIPKDLIDEEKFVVELIVOCIRLSEMPOTHHNALL 1221

QY 1308 LGTYAGIFPPKVLNHNISITFGANVMRLDDTYSFQVINKTVKVMIPALIQSDGDSIE 1367
 DB 1222 LGTYAGIFPPKVLNHNISITFGANVMRLDDTYSFQVINKTVKVMIPALIQSDGDSIE 1281

QY 1368 VSRNVEIIVKIIISVEFDALPHVPEHRRPLIVOLVDTGAEEKFIMTLILLEQVYVTK 1427
 DB 1282 VSRNVEIIVKIIISVEFDALPHVPEHRRPLIVOLVDTGAEEKFIMTLILLEQVYVTK 1341

QY 1428 VLAANGKDALLEADTEFWFSVCCESVOHOIOSLNLIOYLLKLPKEKEETIPRAVSF 1487
 DB 1342 VLAANGKDALLEADTEFWFSVCCESVOHOIOSLNLIOYLLKLPKEKEETIPRAVSF 1401

QY 1488 NKSSEMEMOVNENHTSKOLRHRKFLSVSPMSQLSSNNFLKAVVSGEPILLKGL 1547
 DB 1402 NKSSEMEMOVNENHTSKOLRHRKFLSVSPMSQLSSNNFLKAVVSGEPILLKGL 1461

QY 1548 ERLEETVLYGISVAOASMERNAADLTVEFWRALISKAYDLDBVNALLPETPIPIVIRGL 1607
 DB 1462 ERLEETVLYGISVAOASMERNAADLTVEFWRALISKAYDLDBVNALLPETPIPIVIRGL 1521

QY 1608 VGNPLSVRRKALDLNNKLOONISMKKTIIVTRFLKLVDPDLAIYORK 1655
 DB 1522 VGNPLSVRRKALDLNNKLOONISMKKTIIVTRFLKLVDPDLAIYORK 1569

RESULT 5
 US-08-936-487-52
 Sequence 52, Application US/08936487
 GENERAL INFORMATION:
 APPLICANT: Bowcock, Anne M.
 TITLE OF INVENTION: Compositions and Methods Comprising
 TITLE OF INVENTION: BARD1 and Other BRCA1 Binding Proteins
 NUMBER OF SEQUENCES: 130
 CORRESPONDENCE ADDRESS:
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/936.487
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/025,296

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; FILING DATE: 20-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,611
; FILING DATE: 03-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,985
; FILING DATE: 04-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: P-41,071
; REFERENCE/DOCKET NUMBER: UTSID:499
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-936-487-52

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Query Match      23.9% Score 2586; DB 13; Length 515;
Best Local Similarity 99.0%; Pred. No. 1.2e-197;
Matches 510; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1630 NISMKTIYTRFLKLVDPDLAIYQRRKKEGEEOAINROTALYTLKLCKNGAENPDF 1689
DB 1 NISMKTIYTRFLKLVDPDLAIYQRRKKEGEEOAINROTALYTLKLCKNGAENPDF 60
QY 1690 VPLVTAVKLIAPERKEENKVGSLICIAEYTSLEALAIPOLEPSMLTMTKNTSE 1749
DB 61 VPLVTAVKLIAPERKEENKVGSLICIAEYTSLEALAIPOLEPSMLTMTKNTSE 120
QY 1750 LVSEVYLLSALAALQKVETLPHFISPYLEGISQVHLEKITSMSGASQANIRLISL 1809
DB 121 LVSEVYLLSALAALQKVETLPHFISPYLEGISQVHLEKITSMSGASQANIRLISL 180
QY 1810 KRLATTLAPRVLPVIAIKTKYKQIEKNMKNHMGPPMSIIQEHIGAKKKEELTSHOSQLTA 1869
DB 181 KRLATTLAPRVLPVIAIKTKYKQIEKNMKNHMGPPMSIIQEHIGAKKKEELTSHOSQLTA 240
QY 1870 FLEALDFAHSENDLEEVGKTENCIIQOLVAMVYKLSSEVFRPLFEFLPMKTEDAP 1929
DB 241 FLEALDFAHSENDLEEVGKTENCIIQOLVAMVYKLSSEVFRPLFEFLPMKTEDAP 300
QY 1930 KQRLTFYMLADCIAREKLGFLFLFAGHLVKKPADIIXOVNISKTDEAFDSSENDPEKCC 1989
DB 301 KQRLTFYMLADCIAREKLGFLFLFAGHLVKKPADIIXOVNISKTDEAFDSSENDPEKCC 360
QY 1990 LLLQFLINLKYKFLPDTHFISKERAXALAMPVLVQLENRLGEGEKFOERYTKHLIPCI 2049
DB 361 LLLQFLINLKYKFLPDTHFISKERAXALAMPVLVQLENRLGEGEKFOERYTKHLIPCI 420
QY 2050 APEVSAMADDSLMKPLNYOILKTRDSSPKVRFALITVALAEKIKENVYLLPESIPF 2109
DB 421 APEVSAMADDSLMKPLNYOILKTRDSSPKVRFALITVALAEKIKENVYLLPESIPF 480
QY 2110 LAELMEDECEVEHOCQKTIQOLETVLGEPLQSYF 2144
DB 481 LAELMEDECEVEHOCQKTIQOLETVLGEPLQSYF 515

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; RESULT 6
; US-60-167-217-22825
; Sequence 22825, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CLO000152

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; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22825
; LENGTH: 2147
; TYPE: PRT
; ORGANISM: Drosophila
US-60-167-217-22825

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Query Match      18.6% Score 2012.5; DB 24; Length 2147;
Best Local Similarity 27.9%; Pred. No. 1.6e-150;
Matches 627; Conservative 423; Mismatches 911; Indels 289; Gaps 67;

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QY 14 POSDASLRDEVASLFDPEKATIDRTAFAGCTGLEELGIDPSFEQFEAPLFSQL 73
DB 66 POSDASLRDEVASLFDPEKATIDRTAFAGCTGLEELGIDPSFEQFEAPLFSQL 125
QY 74 AKTERSVQTKAVNKOQDENISLFLHSPYFLKPAQCKLEMLHFRHILNYQDSLIA 133
DB 126 TLTTERSVLPBINKMLDAALAKELRLSPYLLRPAHMAFEWLLRRQVHEYNRSEYMA 185
QY 134 CVLPYHEFRIFRVYIOLKTKNNSKHWFMLPVKOSGVPPLAKGTLYTHCYKDLGFMDFIC 193
DB 186 LILPYHEFRIFRVYIOLKTKNNSKHWFMLPVKOSGVPPLAKGTLYTHCYKDLGFMDFIC 245
QY 194 SLVTKSVKVFVEYPPSSAQLRVLLAFYASTIVSALVAEDVSDNIATKLPYIOLKGLSS 253
DB 246 OSTQKAVR---ELGPRAHQLOAQINFAVTVVAGALQTAKPQDMWHITTLSSLRGLSID 302
QY 254 LPDYAAATYMIICQSVYVYNTFVNSLASQIITKTKIPS-----LIKGLSCLIVLL 308
DB 303 NIDFAAAVYVIAQVLSRTKLSKVCNAL-----LERVNCPEERLHSESLLLVCIT 355
QY 309 QROKESIGKKRPFILCNVDPDLITLHGISEYDVSPLRYMLPRLVYSII-----HHV 362
DB 356 GKO-----QALPAHF--KPE--TILNLVYKKWLISTLSLAKGNIAIOSICMLPTMGAV 405
QY 363 TGEETEGNDGOYIKRHLAELITKISLKNLHLASLFEYIS----- 406
DB 406 AAIRODDASSNCKFLDNLSEVPMPTAQOLINCLDTRYVERAIDAPPEMETSNEED 465
QY 407 -----YSSQEDMSKQVSLNEQPLRLLESKPRFLDVVLEHKEIADLKQELFPH 461
DB 466 DDTIVIDDDDELETKT--FOAWYSTYLEKERRYPFAFDLSYKDALRSKSTSNROKAL 524
QY 462 QPV---SLTSGKTYQFLADSDPTSLMLSLNHPPLAVRILAMNH--LKKIMKTSKEGVDSF 517
DB 525 KIALGFLRLNTDEKAKHAYE-----KLIHYSAWMRLSAVOKLQNLNNTKKRRRSYKL 577
QY 518 IKEAVLARIQDNDIDVLSAIS-AEIFKEHFSSEVTISNLNLFQRAELSKNGEWEVYL 576
DB 578 LOECPLRINDSGAVVSTLLSLPTEELAEMLGPLPLAQIOTCHILYRQOSEKDEEMQV 637
QY 577 KIAAAILKEELISNDQLSQVYVCLLPVYINNDQTESAMKAIYLSGSGISLPL 636
DB 638 PLAVRHLSALVSGSYD--TNLVLLALMPLLEPGBALAEHOKALRILIG--SDFVSKVPF 694
QY 637 LGMEAEALENVIKSTPKGLKIGVANQKMIELLA--DNIMIGDPS--SLMKVIEDLVSGEE 694
DB 695 LA--ELKYSNKSFDN-----VGEHRQHLDIITASSNOELSSOERALLQSDV--HGSEL 745
QY 695 SFNLKQKVTFAVILSVSCSSSLKETHPFAIRVFSLLQKKIKKLESVITAVE-----I 749
DB 746 YLOKASQLT--HLLLLITVYAKRELQPRESIMLEKIGLYSRLO--FRVYNGSQDTQCA 802
QY 750 PSEMHIELMDGIGIVELMAHVEELNSTORAAVDSVFLVSLKFTI-----YALKAKS 805
DB 803 PLQTLVDFLLTL--VKNTKWT-----ALASTPNQMDELRLCIRLEITICAOVFSKAO-- 856
QY 806 FPKGDIMWNPQ-----LKEDSRDYLLHGLFEMWLGACADAVHFRVLMKLIKVIHLEDV 860

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XX PS Disclosure: Page 287-288; 348pp; English.

CC The sequence is that of a protein which can be used in the
 CC preparation of the recombinant breast cancer antigen, BRCA1, binding
 CC proteins BAR1, B123, BE2, BE14, BE31 or BE445, or a composition for the
 CC detection of a BAR1, B123, BE2, BE14, BE31 or BE445 nucleic acid
 CC sequence, specifically a wild type BAR1 composition for the detection
 CC or purification of BRCA1, useful to identify a patient having, or at
 CC risk of developing cancer. BAR1 can be used in the preparation of a BRCA1
 CC anti-BAR1 antibody, and in the detection and purification of a BRCA1
 CC protein. BAR1, B123, BE2, BE14, BE31 or BE445 can be used in the
 CC identification of a binding protein agonist or antagonist that alters
 CC the binding of BAR1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the
 CC biological activity of the BRCA1-BAR1, B123, BE2, BE14, BE31 or BE445
 CC complex. The antibodies can be used to detect BAR1, B123, BE2, BE14,
 CC BE31 or BE445, a specific anti-BAR1 antibody can be used to identify
 CC a patient having or at risk of developing cancer.

XX Sequence 515 AA;

Query Match 23.9%; Score 2585; DB 19; Length 515;
 Best Local Similarity 99.0%; Pred. No. 3.1e-180;
 Matches 510; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1630 NISKKKTVIRFLVLPDLAIYORKKKEGEQAIRGALYTLKLCNFGAENPDPF 1689
 DB 1 NISKKKTVIRFLVLPDLAIYORKKKEGEQAIRGALYTLKLCNFGAENPDPF 1689
 QY 1690 VPIVXTAVKLIAPRKEKKNVIGSALICIAEVTSTLALAIPOLPSPSLTTMKATSE 1749
 DB 61 VPIVXTAVKLIAPRKEKKNVIGSALICIAEVTSTLALAIPOLPSPSLTTMKATSE 1749
 QY 1750 LVSEVYLLSALAALQKRVETLPHFISPILEGILSQVYIHEKIRSEKSAQANIRLTS 1809
 DB 121 LVSEVYLLSALAALQKRVETLPHFISPILEGILSQVYIHEKIRSEKSAQANIRLTS 1809
 QY 1810 KKTATLAPRVILPAIKTKYKQIEKKNKKNMGPSPSILQEHGKMKKEELTSHQSOLTA 1869
 DB 181 KKTATLAPRVILPAIKTKYKQIEKKNKKNMGPSPSILQEHGKMKKEELTSHQSOLTA 1869
 QY 1870 FLEALDFRQHSNDELEVGKTEKNCITDCLVAVVVKLSEVTPPLFEKLPDANKTDPAR 1929
 DB 241 FLEALDFRQHSNDELEVGKTEKNCITDCLVAVVVKLSEVTPPLFEKLPDANKTDPAR 1929
 QY 1930 KDRLLTVYNADCIATKELKGLFTLFGHLVYKPRADTLXQVNIKSTDEAFDSENDPEKCC 1989
 DB 301 KDRLLTVYNADCIATKELKGLFTLFGHLVYKPRADTLXQVNIKSTDEAFDSENDPEKCC 1989
 QY 1990 LLLQFNLNCLYKIFLPTQHFISKERAKALAMPVLDLENKRLGEGEFQERVTKHLIPCT 2049
 DB 361 LLLQFNLNCLYKIFLPTQHFISKERAKALAMPVLDLENKRLGEGEFQERVTKHLIPCT 2049
 QY 2050 AQSVMADSLMKPLNYQLLKTQDSSPVRFPAALITVALAEKLENTIVLLPSPIR 2109
 DB 421 AQSVMADSLMKPLNYQLLKTQDSSPVRFPAALITVALAEKLENTIVLLPSPIR 2109
 QY 2110 LAELMEDCEVEHQCKTQQLQLETVLGEPLQSYF 2144
 DB 481 LAELMEDCEVEHQCKTQQLQLETVLGEPLQSYF 2144

RESULT 2

AA19675 ID AAM19675 standard; Protein; 2932 AA.

AA19675; AC AAM19675;

DT 20-AUG-1997 (first entry)

XX ATW mutant 2467del372.

KM ATM gene; ataxia-telangiectasia; progressive genetic disorder; antibody;
 KM central nervous system; immune system; chromosomal instability; therapy;
 KM cancer predisposition; radiation sensitivity; cell cycle abnormality;
 KM multi-system disease; autosomal recessive; cerebellar ataxia; cerebellum;
 KM general motor dysfunction; Purkinje cell; oculocutaneous telangiectasia;
 KM blood vessel; bulbar conjunctiva; facial skin; A-T; murelin.
 OS Homo sapiens.

XX Key Location/Qualifiers
 XX Key MISC-difference 263 /note="encoded by CTT"
 XX MISC-difference 554 /note="encoded by ACG"
 XX MISC-difference 637 /note="encoded by CAA"
 XX MISC-difference 750 /note="encoded by AAC"
 XX MISC-difference 822..823 /note="site of 124 amino acid deletion"

XX MO9636691-A1.
 XX 21-NOV-1996.
 XX 16-MAY-1996; 96MO-US07025.
 XX 08-APR-1996; 96US-0629001.
 XX 16-MAY-1995; 95US-0441822.

XX (KOHN/) KOHN K I.
 XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Shiloh Y;
 XX WPI; 1997-012070/01.
 XX N-PSDB; AAT68758.

XX New isolated ataxia-telangiectasia gene - used to develop prods. for
 XX the study, diagnosis and treatment of ataxia-telangiectasia.

XX Claim 5; Page -; 153pp; English.

XX AAM19648-W19702 represent mutations of the ATM gene of the invention
 XX (see AAM06234 for wild type sequence). The ATM gene of the invention, is
 XX located in the human genome at chromosome segment 11q22-23.
 XX Ataxia-telangiectasia (A-T) is caused by mutations, insertions, or
 XX deletions (such as represented by this sequence) in the coding region of
 XX the ATM gene. A-T is a progressive genetic disorder affecting the central
 XX nervous and immune systems. A-T involves chromosomal instability, cancer
 XX predisposition, radiation sensitivity, and cell cycle abnormalities. A-T
 XX is a multi-system disease inherited in an autosomal recessive manner.
 XX The wild type gene, can be used in methods for detecting carriers of a
 XX defective gene that causes A-T. The gene can also be used to generate
 XX antibodies. The methods and antibodies can be used in the study,
 XX diagnosis and therapy of A-T.

XX Sequence 2932 AA;

Query Match 2.5%; Score 273; DB 18; Length 2932;
 Best Local Similarity 18.6%; Pred. No. 2.8e-10;
 Matches 411; Conservative 354; Mismatches 777; Indels 662; Gaps 105;

QY 236 DNIIAKLPYIOG---LKSSLPDYRAATYMIQISVYKWTMENTFVNSLSAQITK---- 288
 DB 58 DAVFIRLQKYLQKTECELIAPKPNVSAST---GASRQKKMGE--LSLKYFIKCANR 110
 QY 289 -----TLTKIPSLIKD-----GLSCIVLLQROKPESLGKRPPLHCVNP----- 328
 DB 111 REPIRLKQELLINIDTVKSSNGAIGYAGDSNLIK-----DISVRY--WCESLQGW 164
 QY 329 -DLITILNGISFTYDVSPILRYMLPH-----LVYSIIHVTG---EETEGMDQIYKRH 378

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 15, 2001, 15:12:03 ; Search time 34.51 Seconds

(without alignments)
3766.382 Million cell updates/sec

Title: US-09-603-665-5
Perfect score: 10807
Sequence: 1 MSLAQQLRLALPQSDASL.....CKTIQQLFTVGEPIQSYF 2144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

A.Geneseq.0601.*
1: /SIDSB8/gcgdata/geneseq/geneseqp/AA1980.DAT.*
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22: /SIDSB8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2585	23.9	515	AAW54099	Homo sapiens BAP28
2	273	2.5	2932	AAW19675	ATM mutant 2467del
3	272.5	2.5	2954	AAW01632	Amino acid sequenc
4	271.5	2.5	3055	AAW19697	ATM mutant 5435del
5	270.5	2.5	2989	AAW19688	ATM mutant 1407del
6	262.5	2.4	3059	AAW19696	ATM mutant 5319ins
7	262	2.4	2998	AAW19691	ATM mutant 3403del
8	262	2.4	3046	AAW19690	ATM mutant C9140T
9	262	2.4	3053	AAW19694	ATM mutant 7636del
10	262	2.4	3054	AAW19695	ATM mutant 7279del
11	262	2.4	3055	AAW19693	ATM mutant 8578del

12	262	2.4	3056	AAW19733	Cell cycle checkpo
13	262	2.4	3056	AAW19698	ATM mutant E2904G.
14	262	2.4	3056	AAW19699	ATM mutant Leu43Pr
15	262	2.4	3056	AAW37133	Ataxia-telangiecta
16	262	2.4	3056	AAW84269	Human ataxia-telan
17	261	2.4	2075	AAW19682	ATM mutant 6199del
18	261	2.4	2193	AAW19660	ATM mutant 6573del
19	261	2.4	2415	AAW19686	ATM mutant 7240del
20	261	2.4	2507	AAW19659	ATM mutant 7517del
21	261	2.4	2545	AAW19657	ATM mutant 7630del
22	261	2.4	2598	AAW19656	ATM mutant 7789del
23	261	2.4	2652	AAW19655	ATM mutant 7883del
24	261	2.4	2713	AAW19654	ATM mutant C8140T.
25	261	2.4	2759	AAW19652	ATM mutant 8269del
26	261	2.4	2766	AAW19651	ATM mutant 8283del
27	261	2.4	2768	AAW19650	ATM mutant G8307A.
28	261	2.4	2987	AAW19649	ATM mutant 8946ins
29	261	2.4	3003	AAW19648	ATM mutant 7630del
30	261	2.4	3005	AAW19653	ATM mutant 8269del
31	261	2.4	3021	AAW19661	ATM mutant 6348del
32	261	2.4	3054	AAW19702	ATM mutant 7278del
33	261	2.4	3056	AAW06234	ATM protein. Homo
34	261	2.4	3056	AAW07655	Ataxia-telangiecta
35	261	2.4	3056	AAW07655	ATM mutant G9170C.
36	261	2.4	3057	AAW19701	Human ATM protein.
37	260.5	2.4	2998	AAW19673	ATM mutant 3403del
38	260	2.4	3066	AAW36178	Murine Ataxia-tela
39	259	2.4	3026	AAW19676	ATM mutant 2377del
40	258	2.4	3433	AAW22017	Ulrophin. Homo sa
41	255.5	2.4	3435	AAW19654	Human ATM protein.
42	255	2.4	3056	AAW19653	Arabidopsis thalia
43	254.5	2.4	2825	AAW30671	Arabidopsis thalia
44	254.5	2.4	2837	AAW30670	Arabidopsis thalia
45	254.5	2.4	2895	AAW30669	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAW54099	standard; Protein: 515 AA.
ID	AAW54099	
XX	AAW54099;	
AC		
XX		
DT	28-SEP-1998	(first entry)
XX		
DE	Homo sapiens BAP28 sequence.	
XX		
KW	BARDL; ring protein; BRCA1; breast cancer; risk; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
FN	W09812327-A2.	
XX		
PD	26-MAR-1998.	
XX		
PE	19-SEP-1997;	97WO-US16842.
XX		
PR	04-APR-1997;	97US-0042985.
PR	20-SEP-1996;	96US-0025296.
PR	03-APR-1997;	97US-0042611.
XX		
PA	(TEXA) UNIV TEXAS SYSTEM.	
PI	Baer R. Bowcock AM;	
XX		
DR	WPI; 1998-230317/20.	
DR	N-PSDB; AAV24135.	
XX		
PT	DNA sequence encoding BARDL, B123, BE2, BE14, BE31 or BE445 - which	
PT	as breast cancer antigen, BRCA1, binding proteins are useful to	
PT	identify patient having or at risk of developing cancer	